

**Amendments to the Specification.**

Please amend the specification as shown below.

Please amend the title of the invention as follows by deleting the material indicated by strike-through and adding the underlined material:

-- Method for Lowering Both Sequence Variations ~~Variations~~ and Increase of Base Line ~~Line's~~ Effects in Diagnostic Hybridisation Assay, Assay for Performing Such a Method and Probe for Use in the Assay. --

After the title, please insert the following as a new paragraph:

**--Related Application Information**

This application claims the benefit under 35 U.S.C. § 371 of PCT Application Serial No. PCT/EP2003/013676, filed December 2, 2003, the disclosure of which is incorporated by reference herein in its entirety, which claims the benefit of European Application Serial No. EP 02080125.4, filed December 3, 2002, the disclosure of which is incorporated by reference herein in its entirety.--

Please replace the paragraph at page 13, line 31 to page 14, line 7 with the following rewritten paragraph:

--In this application the terms "analyte", "amplicon" and "target" or "target sequence" ~~analyte~~, ~~amplicon~~ and ~~target~~ or ~~target sequence~~ may be used interchangeably. The analyte is the original nucleic acid molecule to be detected. The target sequence is the part of the analyte that is amplified by means of the primers. The amplification leads to formation of amplicons, which are the nucleic acid molecules that are physically detected by hybridization to the probe. The

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sequence of the amplicons is the same or complementary to the target sequence within the analyte.--

An Abstract of the disclosure is being submitted herewith on a separate sheet.  
Please enter the Abstract as page 30 at the end of the specification.